

Plant Gene Register

Nucleotide Sequence of a cDNA Encoding a Heat-Shock Protein (HSP70) from Barley (*Hordeum vulgare* L.)¹

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Among various so-called heat-shock proteins is a highly conserved family that has an average molecular mass of 70 kD and is known as the HSP70 proteins. Some HSP70s are heat inducible but others are constitutive. HSP70s have been identified in many cellular compartments and function as molecular chaperones with diverse roles in protein metabolism (for review, see Hendrick and Hartl, 1993).

A cDNA library of poly(A)⁺ RNA from 3-d-old pollinated barley ovaries in Uni-ZAP XR was screened with first-strand cDNA probes of poly(A)⁺ RNA from unpollinated and pollinated ovaries, respectively. A 2028-bp cDNA was identified for its elevated level after pollination and converted to Bluescript SK⁻ by in vivo excision. DNA sequence was determined by the dideoxy method of Sanger (Sanger et al., 1977) using an autosequencer (Applied Biosystems, Foster City, CA, model 373A, version 1.2.0). Sequence homology analysis showed that the cDNA clone belongs to the HSP70 family. The predicted amino acid sequence was 87% identical to that of the heat-shock protein from spinach (Anderson et al., 1994). Characteristics pertaining to the barley HSP70 clone are described in Table I.

Elevated mRNA levels were observed after pollination and during early embryogenesis as compared to levels in unpollinated ovaries. Moderate restriction fragment-length polymorphisms were detected for the HSP70 locus in the genomic DNA blots of five barley cultivars (Dicktoo, Morex, Steptoe, Harrington, and TR306). Using the barley genome mapping population of Steptoe × Morex (Kleinhofs et al., 1993), the HSP70 locus was mapped to the plus arm of barley chromosome 6, 3.8 centimorgans from the carboxypeptidase locus (Kleinhofs et al., 1993).

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Abbreviation: HSP70, 70-kD heat-shock protein.

Table I. Characteristics of a cDNA encoding the HSP70 of barley

Organism:	Barley (<i>Hordeum vulgare</i> L. cv Morex).
Genome Location:	Plus arm of barley chromosome 6.
Gene Function:	An HSP70 that functions as a molecular chaperone.
Source:	cDNA of poly(A) ⁺ RNA from 3-d-old pollinated barley ovaries.
Sequencing Technique:	Dideoxy chain-termination method.
Method of Identification:	Sequence comparison with GenBank, EMBL, and SwissProt data bases.
Expression Characteristics:	The mRNA levels are up-regulated during early embryogenesis.
Features of Predicted Amino Acid Sequence:	An open reading frame encodes a 608-amino acid protein with a predicted molecular mass of 67,015 D and an isoelectric point of 5.8.
Antibodies:	None.

The GenBank accession number for the sequence reported in this article is L32165.

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